WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a sequence as set forth in SEQ ID NO:1 and variants thereof having at least 70% identity to SEQ ID NO:1 and encoding a polypeptide having polymerase activity at a temperature in a range from about 90°C to 113°C.

2. The isolated nucleic acid of claim 1, wherein the polymerase activity is retained at the temperature for four or more hours.

3. The isolated nucleic acid of claim 1, comprising a sequence as set forth in SEQ ID NO: 1, sequences substantially identical thereto, and sequences complementary thereto.

4. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of high stringency.

5. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of moderate stringency.

6. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of low stringency.

7. An isolated nucleic acid having at least 70% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

8. An isolated nucleic acid having at least 80% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

9. An isolated nucleic acid having at least 90% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

10. An isolated nucleic acid having at least 95% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

11.   The isolated nucleic acid of claim 7, 8, 9, or 10, wherein the sequence comparison algorithm is FASTA version 3.0t78 with the default parameters.

12.   An isolated nucleic acid comprising at least 10 consecutive bases of a sequence as set forth in SEQ ID NOs: 1, sequences substantially identical thereto, and sequences complementary thereto.

13.   An isolated nucleic acid having at least 70% homology to the nucleic acid of claim 11 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

14.   An isolated nucleic acid having at least 80% homology to the nucleic acid of claim 11 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

15.   An isolated nucleic acid having at least 90% homology to the nucleic acid of claim 11 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

16.   An isolated nucleic acid encoding a polypeptide having a sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto.

17.   An isolated nucleic acid encoding a polypeptide comprising at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO: 2, and sequences substantially identical thereto.

18.   A purified polypeptide having at least 70% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

19.   A purified polypeptide having at least 80% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

20.   A purified polypeptide having at least 90% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

21.   A purified polypeptide having at least 95% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

22.   A purified polypeptide having at least 70% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

23.   A purified polypeptide having at least 80% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

24.   A purified polypeptide having at least 90% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

25.   A purified polypeptide having at least 95% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

26.   A purified polypeptide having a sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto, wherein the polypeptide has polymerase activity at temperatures in the range from about 70°C up to about 113° C.

27.   An assay for identifying functional polypeptide fragments or variants encoded by fragments of SEQ ID NO: 1, and sequences substantially identical thereto, that retain the polymerase function of the polypeptide of SEQ ID NO: 2, and sequences substantially identical thereto, said assay comprising:

        utilizing a polypeptide encoded by a nucleic acid having at least 70% homology to SEQ ID NO: 1, and sequences substantially identical thereto, or polypeptide

fragment or variant encoded by SEQ ID NO: 1, to effect DNA polymerase activity in a PCR amplification at extreme high temperature for four or more hours and under conditions that allow said polypeptide or fragment or variant to function, and

detecting formation of an amplification product, wherein formation of the amplification product is indicative of a functional DNA polymerase polypeptide or fragment or variant.

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